



PCT09

RAW SEQUENCE LISTING

DATE: 06/12/2002

PATENT APPLICATION: US/09/913,064A

TIME: 14:49:28

Input Set : A:\BB1321-1 US PCT SEQ LIST.txt

Output Set: N:\CRF3\06122002\I913064A.raw

3 <110> APPLICANT: Carlson, Thomas J.
 4 Fader, Gary M.
 5 Famodu, Omolayo O.
 6 Kinney, Anthony J.
 7 Pearlstein, Richard W.
 8 Rafalski, J. Antoni
 9 Thorpe, Catherine J.
 11 <120> TITLE OF INVENTION: UDP-Glucose Modifiers
 13 <130> FILE REFERENCE: BB-1321-1
 15 <140> CURRENT APPLICATION NUMBER: 09/913,064A
 16 <141> CURRENT FILING DATE: 2002-04-15
 18 <150> PRIOR APPLICATION NUMBER: PCT/US00/03453
 19 <151> PRIOR FILING DATE: 2000-02-09
 21 <150> PRIOR APPLICATION NUMBER: 60/119,588
 22 <151> PRIOR FILING DATE: 1999-02-10
 24 <160> NUMBER OF SEQ ID NOS: 28
 26 <170> SOFTWARE: Microsoft Office 97
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 509
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Zea mays
 33 <220> FEATURE:
 34 <221> NAME/KEY: unsure
 35 <222> LOCATION: (413)
 36 <223> OTHER INFORMATION: n = A, C, G, or T
 38 <220> FEATURE:
 39 <221> NAME/KEY: unsure
 40 <222> LOCATION: (465)
 41 <223> OTHER INFORMATION: n = A, C, G, or T
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 44 <221> NAME/KEY: unsure
 45 <222> LOCATION: (485)
 46 <223> OTHER INFORMATION: n = A, C, G, or T
 48 <400> SEQUENCE: 1
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 50 tgtcattcac ttcgctggat tgaaagctgt gggtgaaaagc gtacagaagc cattacttta 120
 51 ttatgacaac aacgtcattg gcacgataaa tcttctagaa gttatgtctg ttcacggttg 180
 52 caagaagttg gtgttctcat catcagctgc agtttatgga tccccaaaa actcaccttg 240
 53 cacagaaaat tttcctctta ctccaaacaa tccatatggc aaaacaaagc tcgttgttga 300
 54 agatatttgc cgggatattc accgttcaga tcctgaatgg aagatcattt tacttaggta 360
 55 cttcaatcca gttgggtgctc atcctagtgg atatccttggc gaggaccac gangaattcc 420
 56 caacaatctt atgccctatg ttcagcaagt tgcggttggt aagangccag ctctaacagt 480
 57 tttangaaat gactatgcaa caagagatg 509

ENTERED

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59 <210> SEQ ID NO: 2
60 <211> LENGTH: 169
61 <212> TYPE: PRT
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65 <221> NAME/KEY: UNSURE
66 <222> LOCATION: (138)
67 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
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70 <221> NAME/KEY: UNSURE
71 <222> LOCATION: (155)
72 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
74 <220> FEATURE:
75 <221> NAME/KEY: UNSURE
76 <222> LOCATION: (162)
77 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
79 <400> SEQUENCE: 2
80 Ile Asp Leu Arg Asp Lys Gly Ala Leu Glu Met Val Phe Ala Ser Thr
81   1           5           10           15
83 Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly Glu
84           20           25           30
86 Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Val Ile Gly Thr
87   35           40           45
89 Ile Asn Leu Leu Glu Val Met Ser Val His Gly Cys Lys Lys Leu Val
90   50           55           60
92 Phe Ser Ser Ser Ala Ala Val Tyr Gly Ser Pro Lys Asn Ser Pro Cys
93   65           70           75           80
95 Thr Glu Asn Phe Pro Leu Thr Pro Asn Asn Pro Tyr Gly Lys Thr Lys
96           85           90           95
98 Leu Val Val Glu Asp Ile Cys Arg Asp Ile Tyr Arg Ser Asp Pro Glu
99   100          105          110
101 Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro
102   115          120          125
W--> 104 Ser Gly Tyr Leu Gly Glu Asp Pro Arg Xaa Ile Pro Asn Asn Leu Met
105           130           135           140
W--> 107 Pro Tyr Val Gln Gln Val Ala Val Gly Lys Xaa Pro Ala Leu Thr Val
108 145           150           155           160
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111           165
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114 <211> LENGTH: 456
115 <212> TYPE: DNA
116 <213> ORGANISM: Oryza sativa
118 <220> FEATURE:
119 <221> NAME/KEY: unsure
120 <222> LOCATION: (322)
121 <223> OTHER INFORMATION: n = A, C, G, OR T
123 <220> FEATURE:
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125 <222> LOCATION: (352)
 126 <223> OTHER INFORMATION: n = A, C, G, OR T
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 145 <222> LOCATION: (452)
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 150 gcacacaaca acaacaagag taatcaaagt agaagaagat ggtttcggcc ttgttgcgga 120
 151 cgatcctggt gacggcggc gccggctaca tcggcagcca caccgtcctc cagcttctcc 180
 152 aactcggett ccgctgtgtc gtcctcgaca acctcgacaa cgctcccgag ctgcccattcc 240
 153 tccgcgtcag ggaactcgcc ggacacaacg ccaacaacct cgacttcgc aagggtgacc 300
 154 tccgcgacaa gcaagcgttg gnccaaatct tctctctca aaagggtgag gntgtcatcc 360
 155 aatttgccgg gctgaaaact gttggcgaaa ncgtgaaaaa cccctngttt tacgaaacaa 420
 W--> 156 tcatcggac ataaccact gcagggnata gnggca 456
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 159 <211> LENGTH: 99
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 163 <220> FEATURE:
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 180 <222> LOCATION: (97)
 181 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
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185      1          5          10          15
187 Val Leu Gln Leu Leu Gln Leu Gly Phe Arg Val Val Val Leu Asp Asn
188      20          25          30
190 Leu Asp Asn Ala Ser Glu Leu Ala Ile Leu Arg Val Arg Glu Leu Ala
191      35          40          45
193 Gly His Asn Ala Asn Asn Leu Asp Phe Arg Lys Gly Asp Leu Arg Asp
194      50          55          60
W--> 196 Lys Gln Ala Leu Xaa Gln Ile Phe Ser Ser Gln Lys Val Glu Xaa Val
197      65          70          75          80
W--> 199 Ile Gln Phe Ala Gly Leu Lys Thr Val Gly Glu Xaa Val Lys Asn Pro
200      85          90          95
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208 <213> ORGANISM: Glycine max
210 <220> FEATURE:
211 <221> NAME/KEY: unsure
212 <222> LOCATION: (17)
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216 <221> NAME/KEY: unsure
217 <222> LOCATION: (19)
218 <223> OTHER INFORMATION: n = A, C, G, OR T
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228 <223> OTHER INFORMATION: n = A, C, G, OR T
230 <220> FEATURE:
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232 <222> LOCATION: (48)
233 <223> OTHER INFORMATION: n = A, C, G, OR T
235 <220> FEATURE:
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248 <223> OTHER INFORMATION: n = A, C, G, OR T
250 <220> FEATURE:

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268 <223> OTHER INFORMATION: n = A, C, G, OR T
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272 <222> LOCATION: (369)
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276 <221> NAME/KEY: unsure
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278 <223> OTHER INFORMATION: n = A, C, G, OR T
280 <220> FEATURE:
281 <221> NAME/KEY: unsure
282 <222> LOCATION: (446)
283 <223> OTHER INFORMATION: n = A, C, G, OR T
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W--> 287 gngggnggcg gtttcattgg nacccacacc gtcgttcanc ttctcaaagc tggttcagc 120
288 gtttcaataa tcgacaattt cgataactcc gtcatggaag caatggaccg cgtccgccaa 180
W--> 289 gtggttggn cctctgctttc tcaaaacctc caattcaccc aaggngatct ccggaatagg 240
290 gatgaacttg agaaactctt ctccaaaaca acatttgatg ccgtgatcca ctttgctggc 300
W--> 291 ttgaaaagcg gttgctgaaa gcgttgcgaa accccgtcgc tattttgatt ttaatttggn 360
W--> 292 tgggaccanc aacctctacg agtttatggn aaagtataat tgcaaaaaga tgggtttctc 420
W--> 293 atcatctgca accgtttatg ggcaanctga aaaaataccg tgtgaggagg attcaagtt 479
295 <210> SEQ ID NO: 6
296 <211> LENGTH: 148
297 <212> TYPE: PRT
298 <213> ORGANISM: Glycine max
300 <220> FEATURE:
301 <221> NAME/KEY: UNSURE
302 <222> LOCATION: (3)
303 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
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307 <222> LOCATION: (7)
308 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
310 <220> FEATURE:

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